

[illegible]

1931 CTCTAATAAATAATATAGCCGGCCAGGAAAAAATAAATAAATAAATAA

Figure 3

10 20 30 40 50 60 70 80 90 100 110 120
GAATTCATCGTGGCAAGGGCAGCCTGAATGGATGATGTAACCTGGGGTCCTTTCAATGGAGGGCCAGACTCCTGGGTCTAGGGGATGAGGGAGGGGAGGATCGGGTTAGCTGGGACCA

130 140 150 160 170 180 190 200 210 220 230 240
GGTGAAGAGGGGCTGGGGGGCCACATTCTGAGTCTCAGAGAGAAGGATCTGGGGTCTCAAGCACCTGAGTCGGAGGGAGGAGGGGTGCTGGGCTCCTGAAAAACCACCTCTTGGACCAT

250 260 270 280 290 300 310 320 330 340 350 360
CTATGCAGATCAGCAGAACAGAGAAATTTCTGCGCCCATCTGAATTTCTAAGTTTGGGGGGAGGGCGTGATCTGACACTGAGGTTCTTGATCCTCAGCAAGGGGCAATTGCTGTA

370 380 390 400 410 420 430 440 450 460 470 480
TGAAGAAGCGACCGCATCTGAGACACAAGTATCCTGCCTTGAAGCCTCTCACCTGGCCGTGGGCCAACCTCAACCTCATCTGTCCCTGCTCAGATGCTCAGACCTGGACATCCAGC

490 500 510 520 530 540 550 560 570 580 590 600
CTCCTCCTCCCTGATGCAATCCTGGTGTCTTTTACCAGAGAAGCCATCCAGGGCCAGGCAGGTGCTCCTGAAATAACCTGGGGGAGGGGTGGCTGAAAGTCCCTGACTGGAGTTGG

610 620 630 640 650 660 670 680 690 700 710 720
CAGCCAAGCCAGGCCCTGGAGTGGGCACCCAGAGGAAGACAGGTGGCTAATTTCTGGAGCCCTAAGGGTGCAAGGGTAGGCCTTCTGTGCTCAGGGAGGAGGGCTGGGGCTCTGG

730 740 750 760 770 780 790 800 810 820 830 840
ACTCCTGGGTCTGAGGGAGGAGGGGTGGGGGGCCTGGACTCCTGGGTCTGAGGGAGGAGGGTCTGGGCCTGTA CTCTGGATCTGAGGGAGGAGGGGTGGGGAAC TTGGGCTCCTGGGT

850 860 870 880 890 900 910 920 930 940 950 960
CTGAGGGAGGAGGGAGCTTTGGTCTGGACTCCTGGGTCTGAGGGAGTAGGGGCTAGGGATCTGGACTCGTGGGTGTGAGGAAGGAGGGGCTGGGGTCTGGACTCCTGGGTCTGAGGAAG

970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080
GAGGGGAGGGGGCTTGGACTCCTGGGTCTGAGGAAGGAGGGGCCGGGAGCCTGGACTCCTAAGTCTGAGGGAGGAGGGTCTGGGGCCTGGACTGCTGGGTGTGAGCAGAAAGGTCTGG

1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
GTGCTGGGAGTCCCGAGCCTGGGGAGATGATGGTTAACTTCTGGGAATCAAGTCAAACCTCCTGAGTCTTTGACATTGATGTATCTTGAATGGGAGGGTCAGTCTGTGGGGAAGGATTAC

1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320
CCAGGTGCCGAGGCAAGAGACTGAAGGCACAACTGTTTCAGTATAATAAGAAAAATAGTTAGAATAAGAAATAGTTATCATACAAATTAGATATAGAGATGATCATGGACAGTATCAATC

1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440
ATTAGTGTAACATTATTAATCATTAGCTATTACTTTTATTCTTTGTTGTATAACTAATATAACCAGGAAACAACCGGTGGGTATAGGGTCAGGTACTGAAGGGACATTGTGAGAAGTGA

1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
CCTAGAAGGCAAGAGGTGAGCCTTCTGTACACCGGCATAAGGGCCTCTTGAGGGCTCCTTGGTCAAGCGGGAACGCCAGTGTCTGGGAAGGCACCCGTTACTCAGCAGACCACGAAAGG

1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680
GAATCTCCTTTTCTTGAGGAGTCAAGGAACTCTGCTCCACCAGCTTCTTGTGGGAGGCTGGGTATTATCTAGGCCCTGCCCGCAGTCATCCTGCTGTGCTGTGCTTCAATGGTCACGC

1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800
TCCTTGCTCCTCTTGCAATTTTCTCCCGTACTCCTGGTTCCTCTTTGAAGTTCGTAGTAGATAGCGGTAGAAGAAATAGTGAAGCCCTTTTTTTTTTTTTTTTGAAGCGGAGTCTCGCTC

Figure 3 (cont'd)

Sequence III (cont.)

1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920
TGTCCTCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAATCTCCGCTCCTGGGTTACACCATTCTCCTGCCTCACCCTCCCAAATAGCTAGGACTACAGGGCCCTCCACC											
1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040
ACGGCGCCGGATAATTTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGTTAGCCAGGATGGCCTCCACCTCCTGACCTTGTGATCCGCCCCCTCAGCCTCCCAAAGTGCTGGGATT											
2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160
ACAGGCGTGAGCCACCGCGCCCGCCGAAATAGTGAAAGTCTTAAAGTCTTTGATCTTTCTTATAAGTGCAGAGAAGAAAACGCTGACATATGCTGCCTTCTCTTTCTGCTTCGGCTGCC											
2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280
TAAAGGGGAAGGGCCCTGTCCATGATCACGTGACTTGCTTGACCTATCAGTCATTGGACGACTCACCCTCCTTATCCTGCCCCCTTGTCTTGATACAATAAATATCAGCGCG											
2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
CCAGCCATTTCGGGGCCACTACCGGTCTCTGCGTCTTGATGGTAGTGGTCCCCGGGGCCAGCTGTTTTCTCTTTATCTTTGTCTTGTGCTTTATTTCTTACAATCTCTCCTCTCCT											
2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520
CACAGGGGAAGAACACCCACCCGAAAGCCCGTAGGGCTGGACCTACGTTAGCCTGCCCTGCTCGGGTTGGCGATGCTGGAGGTGGGCCTTGGACCAGAGAAAATGCTTTAATTAGG											
2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640
TGACAAGCGGGCAGAGGCCTTTGTCTCTGCGCGCGCAGCCACGGCCCCGCTGACGGCGTGGGAAACAGACCCTGTTCCACTCCGGTCTCCAGCCTTGAATGGTTGCCTTCGTGCGAT											
2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760
GCAGGTCTGGAAGTAGCAGTTTGGCAGGGACCTAGAATTCCCCAAAGGAGTGACTAGGGGCTGGGATTCTGGAATTTGAGTGTGGACGGTGAGGCGGGGGTGTGGGAGATCGGAG											
2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880
ACCTTGGTGGGCGGGGAGCACCTGCAGGCTGGAGGCCCTCGCGCGCTCCGGCGGCAGCCTGGCAAACAGGTTCTCCATCCCCAGGAGGACGGGCAGAGGGCGGACGATCGCTCCACT											
2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000
CGCCGGGACCAAGGTGCGGGGGCCCTGCCAGCCGCTGGGGCGTGGCCAGGCTCGAAGCACCCAGGTGTGCGGGGGCCGACTCTAAGCCCTGGCACCGGAAGAGAGGGCGGGGATTGGA											
3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120
CCTCCCGGCTCCAGCATTGCAACTGGGCGCTCCGTCTCCTGGTCCACGCAATGATGCTGCGGCTGCTCAGAAGCCAGGTAGCCTGCCCTGGGTGAAGCCTTCGCGCAGGTCAATGACGGG											
3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240
GCGGAGGGGCAGGGCGCGTCCCCTGCATCCCCGATCTGGGAGCGGTGGGCCAGGGGCCATCGCCTTAGCCCTGGCGCTGGGGCTCGGGCCCAAGTGACGGGCGGGGCTCCACCTTC											
3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360
CAGCCATCCGCCCGCCGGGAGGGCGGACGCTGCGAGACTCCGGCCGCGCCCTCTCCTTCTCTCTCCCAAGCCCTCGTGCCAGTCCGGACAGGCTGCGCGGAGGGGAGGGCTGC											
3370	3380	3390	3400	3410	3420	3430	3440	3450	3460	3470	3480
CGGGCGGGATAGCCGGAGCCTGGCGTTCCAGGGGCGGGCGGATGTGGCCTGCTTTGCGGAGGGTGCGCTCCGGCCACGAAAAGCGGACTGTGGATCTGCCACCTGCAAGCAGCTCGGG											
3490	3500	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600
TAAGTGGGACTGCCCACTCAGTTGTTCTGGGACCCAGGAACAATCCTTCAGAACAGGAGGTGCACCCCAACCTCTTCTCAGGTCTTCTAAGGCCCTAGGAATCTCGGCCACC											

Figure 3 (cont'd)

3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720
TCCCCAGCCATTACTCCTCCAGGAACCAAGATGCTCCTTCCGCTCCTGACCCTCCAGCCTCTCTTGTGTTTACTTGAACATATCGTTTCCCATCACCACCTCTGTGGTGGATTTTGC GCCTC

3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840
ACAGACAGGTA CTCTGAGAAACAGGCTGGTGGAGAGTCCAGTATCAGCGGAACCTTACAGGAGGGGAGACTCGAGATTCCTTCAGGAAAGGTGTAGGAACCTGGACCCTTTCTTTTTT

3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960
TTTTTTTTTTTTTTTAAAGACAGGGTCCCTCTCTGTGCGCAAGCTGGAGTGCAGTCAGCGGTGCTATCGCGGCTCATTGTGAGCTCCGGGGATCCTCCCGCCTTAGCATCCGGTGTAG

3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080
CTGAGACCACAGACATGTGCCACCATGCCAAGCTAATTTATTTATTTTGGAGACGGAGTTTCACTCTTGTGCCCAGGCTGGAGTGTAAATGGCATGATCTCAGCTCACCGCAAC

4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200
TCCCCCCCCCGGGTTCAGGCGATTCTCCTGCCTCAGCCTCCCGAGTGGCTGGGATTACAGGCAATGCCACCATGCCCGGCTAATTTGTATTTTAAAGTAGAGACAGGGTTTCTCCACG

4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320
TTGGTCAGGCTGGTCTCGAACTCCCAACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGTGGGATTACAGGTGTGAGCCACCGCGCTGGCCCATGCCAAGCTAATTTTAAATTT

4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440
TTTTTGTAAGAGTCTCTGTTGCCAGGCTGATCTTGAACCTCGTGGGTCAAGGGATCCTCCCATCTCAGCCTCCCAATATGCTGGGATTACAGGTGTGAGCCACAGTGGCCAGCCAAAC

4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560
CATGGCTATCTTGAAACCACTTGTCTTCCAGTCCCCATGCCCCGAAATTCAAAGGCTCTCATCCCTGAAACCTAGGACTCAGGCTCTCCCTACCTCAGCCCCAGGAGTCTAAACCTTTA

4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680
ACTTCCTCTTCCCTGGGACTAAGGAGTGTGACCCCCAGGCGCCTCCCTTACCCACATCCCTCCTCAGCCTCCCTCCTCAGCCTCAGTGCATTGCTAATTCGCTTTCTCCCTCG

4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800
CAGCCATGTGGCTCCGAGCCATCGTCAGCTCTGCTGGCCTTCTGCTAGTCTGTGCTCTCTGTAATCTTCTTCCATATCCATCAAGACAGCTTCCACATGGCCTAGGCCTGT
MetTrpLeuArgSerHisArgGlnLeuCysLeuAlaPheLeuLeuValCysValLeuSerValIlePhePheLeuHisIleHisGlnAspSerPheProHisGlyLeuGlyLeuS

4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920
CGATCTGTGTCCAGACCGCGCCTGGTGACACCCCACTGGCCATCTTCTGCTGCGGGTACTGCGATGGGCCCCAACGCCTCCTCTTCTGTCCCCAGCACCTGCTTCCCTCTCCG
erileLeuCysProAspArgArgLeuValThrProProValAlaIlePheCysLeuProGlyThrAlaMetGlyProAsnAlaSerSerSerCysProGlnHisProAlaSerLeuSerG

4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040
GCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGCTGCTGGCTCTGGCCCACTCAACGGCCGCGGGCCTTTATCCTGCTGCCATGCATGCCG
lyThrTrpThrValTyrProAsnGlyArgPheGlyAsnGlnMetGlyGlnTyrAlaThrLeuLeuAlaLeuAlaGlnLeuAsnGlyArgArgAlaPheIleLeuProAlaMetHisAlaA

5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160
CCCTGGCCCCGGTATTCGATCACCCTGCCCGTGTGGCCCCAGAGTGGACAGCCGACCGCGTGGCGGGAGCTGCAGCTTCAGGACTGGATGTCCGAGGAGTACGCGGACTTGAGAG
laLeuAlaProValPheArgIleThrLeuProValLeuAlaProGluValAspSerArgThrProTrpArgGluLeuGlnLeuHisAspTrpMetSerGluGluTyrAlaAspLeuArgA

5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280
ATCCTTTCTGAAGCTCTCTGGCTTCCCTGCTCTTGACTTTCTTCCACCATCTCCGGGAACAGATCCGAGAGAGTTACCTTGACGACCACCTTCGGGAAGAGGCGCAGAGTGTGC
spProPheLeuLysLeuSerGlyPheProCysSerTrpThrPhePheHisHisLeuArgGluGlnIleArgArgGluPheThrLeuHisAspHisLeuArgGluGluAlaGlnSerValI

5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400
TGGGTGAGCTCCGCTGGCGCCACAGGGGACCGCCCGCACCTTTGTCGGCTCCACGTGCGCGTGGGACTATCTGCAGGTATGCTCAGCGCTGGAAGGGTGTGGTGGCGGACA
euGlyGlnLeuArgLeuGlyArgThrGlyAspArgProArgThrPheValGlyValHisValArgArgGlyAspTyrLeuGlnValMetProGlnArgTrpLysGlyValValGlyAspS

Figure 3 (cont'd)

5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520
 GCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCGTTTTCTGGTCAACAGCAACGGCATGGAGTGGTAAAGAAAACATCGACACCTCCCAGGGCGATG
 erAlaTyrLeuArgGlnAlaMetAspTrpPheArgAlaArgHisGluAlaProValPheValValThrSerAsnGlyMetGluTrpCysLysGluAsnIleAspThrSerGlnGlyAspV

5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640
 TGACGTTTGGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAGTGAACCCACACCATATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTG
 alThrPheAlaGlyAspGlyGlnGluAlaThrProTrpLysAspPheAlaLeuLeuThrGlnCysAsnHisThrIleMetThrIleGlyThrPheGlyPheTrpAlaAlaTyrLeuAlaG

5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760
 GCGGAGACACTGTCTACCTGGCCAACTTCACCTGCCAGACTCTGAGTTCTGAAGATCTTTAAGCCGGAGGGCGCTTCCTGCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCAC
 lyGlyAspThrValTyrLeuAlaAsnPheThrLeuProAspSerGluPheLeuLysIlePheLysProGluAlaAlaPheLeuProGluTrpValGlyIleAsnAlaAspLeuSerProL

5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880
 TCTGGACATTGGCTAAGCCTTGAGAGCCAGGGAGACTTCTGAAGTAGCCTGATCTTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCTGGCATCTTCTGGAGAAGCTTGTGGTGTTC
 euTrpThrLeuAlaLysProEnd

5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000
 TGAAGCAATGGGTGCCGTATCCAGAGTGATTCTAGTTGGGAGAGTTGGAGAGAAGGGGGACGTTTCTGGAAGTGTCTGAATATTCTAGAACTAGCAAAACATCTTTTCTGATGGCTG

6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120
 GCAGGCAGTTCTAGAAGCCACAGTGCCACCTGCTCTTCCAGCCCATATCTACAGTACTTCCAGATGGCTGCCCCAGGAATGGGGAAGTCTCCCTCTGGTCTACTCTAGAAGAGGGGT

6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240
 TACTTCTCCCTGGGTCTCCAAAGACTGAAGGAGCATATGATTGCTCCAGAGCAAGCATTACCAAGTCCCCTTCTGTGTTTCTGGAGTGATTCTAGAGGGAGACTTGTCTAGAGAGG

6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360
 ACCAGGTTTGTGCTGTGAAGAACCCTGCAGGGCCCTTATGGACAGGATGGGGTTCTGGAATCCAGATAACTAAGGTGAAGAATCTTTTAGTTTTTTTTTTTTTTTGGAGACAG

6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480
 GGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGTGATCTTGGCTCACTGCAACTTCCGCCTCCTGTGTTCAAGCGATTCTCCTGTCTCAGCCTCCTGAGTAGATGGGACTACAGGC

6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600
 ACAGGCCATTATGCCTGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTACCATTGTTGGCCGGGATGGTCTCGATCTCCTGACCTTGTCATCCACCTGTCTTGGCCTCCCAAAGTGC

6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720
 TGGGATTACTGGCATGAGCCACTGTGCCAGCCCGGATATTTTTTTAATTATTTATTTATTTATTTATTTATTTAGACGGAGTCTTGCTCTGTAGCCAGGCCAGAGTGCAGTGGCGC

6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840
 GATCTCAGCTCACTGCAAGCTCTGCCTCCGGGTTTCATGCCATTCTGCCTCAGCCTCCTGAGTAGTGGGACTACAGGCGCCCGCCACCAGCCCGGCTAATTTTTTTGTATTTTTAGT

6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960
 AGAGACGGGGTTTCATCGTGTTAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCTGCCACCTCGGCCTCCACAGTGCTGGGATTACCGGCGTGAGCCACCATGCCTGGCCCGGAT

6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080
 AATTTTTTTAATTTTTGTAGAGACGAGGTCTTGTGATATTGCCAGGCTGTTCTCAACTCCTGGGCTCAAGCAGTCTCCACCTTGGCCTCCAGAAATGCTGGGTTTATAGATGTG/

7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200
 GCCAGCACACCGGGCCAAGTGAAGAATCTAATGAATGTGCAACCTAATTTAGCATCTAATGAATGTTCCACCATTTGCTGGAAAAATTGAGATGGAAAAACAAACCATCTCTAGTTGGCC/

[illegible]

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
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910	920	930	940	950	960
CCTTG ACGAC AAGGG	CCTTG GGGGG	GGCCA CATCT	TCATC TTTGG	TTTAT GAGTC	CTGTG
970	980	990	1000	1010	1020
CGTCT TGSTA CAAGC	AATAC TACTA	TGAGC CGGCA	AGTCA GACTT	ATTTG STAGG	GGACC
1030	1040	1050	1060	1070	1080
AAAGG AAAGA ACATG	TTTTG ATTGC	TAAGA AAACA	TTTTG TTCTC	TATCC TTTAC	TGGGC
1090	1100	1110	1120	1130	1140
TGGCA GGCAA AGGAA	ATGTT CTTAT	GAGCA CTCAC	ATTGA AAAC	TAACT TAAGT	TCTTC ACCAA
1150	1160	1170	1180	1190	1200
ATGCA GAGAC TGTCA	AGGCC AGCCC	GCTGC GGGCT	GCCTC GACAA	TTGSA CGCTC	TCGGC
1210	1220	1230	1240	1250	1260
GGGCC ACGAG ATCCT	GGCCA CGGAT	GCGGT GGCCG	CGCCT CTGCT	CGCAC GTTCC	CCCGG
1270	1280	1290	1300	1310	1320
CCTCT GGAAT GCCTC	GCTCC CTCAA	TCCCT CCCTC	CGGCG GGGCT	CGCTG GCGGG	TGGCT
1330	1340	1350	1360	1370	1380
AGGCC CAACG GCAGG	AAGCC GACGC	TATCC TCCGT	TCCGC GGGCG	CGGGT CCGCC	TTCCG
1390	1400	1410	1420	1430	1440
TCTGT TCTAG GGCCT	GCTCC TGCGC	GGCAG CTGCT	TTAGA AGGTC	TCGAG CCTCC	TGTAC
1450	1460	1470	1480	1490	1500
CTTCC CAGGG ATGAA	CCGGG CCTTC	CCTCT GGAAG	GCGAG GGTTC	GGGCC ACAGT	GAGCG
1510	1520	1530	1540	1550	1560
AGGGC CAGGG CGGTG	GGCGC GCGCA	GAGGG AAACC	GGATC AGTTG	AGAGA GAATC	AAGAG
1570	1580	1590	1600	1610	1620
TAGCG GATGA GGGCG	TTGTG GGGCG	CGGCC CGGAA	GCCCT CGGGC	GCGGG CTGGG	AGAAG
1630	1640	1650	1660	1670	1680
GAGTG GCGCG AGGCG	CGCCA GGAGG	CTCCC GGGGC	CTGGT CGGGC	CGGCT GGGCC	CCGGG
1690	1700	1710	1720	1730	1740
CGCAG TGGAA GAAAG	GGACG GGGCG	TGCCC GGTTC	GGCGT CCTGG	CCAGC TCACC	TTGCC
1750	1760	1770	1780	1790	1800
CTGGC GGCTC GCGCC	GCCCC GCACT	TGGGA GGAGC	AGGGC AGGGC	CGGCG GCCTT	TGCAT

100

Variable	Unit	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	Years	35.2	12.5	18	65	0.15	3.2	0.98
Gender	Male/Female	1.2	1.1	0	2	0.05	2.1	0.99
Marital Status	Married/Single	1.5	1.0	0	2	0.10	2.5	0.97
Education	Years	12.8	2.1	8	16	0.20	3.5	0.96
Income	\$/Month	1500	500	500	3000	0.30	4.0	0.95
Health Status	Good/Bad	1.8	0.8	1	2	0.02	2.0	0.99
Stress Level	Low/High	1.3	0.7	1	2	0.08	2.3	0.98
Work Hours	Hours/Week	40.5	8.2	20	60	0.12	3.1	0.97
Job Satisfaction	1-5 Scale	3.2	1.0	1	5	0.18	3.3	0.96
Life Satisfaction	1-5 Scale	3.5	1.1	1	5	0.22	3.6	0.95
Depression Score	0-10 Scale	2.1	1.5	0	10	0.25	3.8	0.94
Resilience Score	0-10 Scale	6.8	2.0	3	10	0.10	3.0	0.97
Self-Esteem Score	0-10 Scale	7.2	2.1	4	10	0.08	2.9	0.98
Optimism Score	0-10 Scale	7.5	2.2	4	10	0.05	2.8	0.99
Gratitude Score	0-10 Scale	7.8	2.3	4	10	0.03	2.7	0.99
Life Purpose Score	0-10 Scale	8.1	2.4	4	10	0.02	2.6	0.99
Meaning in Life Score	0-10 Scale	8.4	2.5	4	10	0.01	2.5	0.99
Existential Well-being Score	0-10 Scale	8.7	2.6	4	10	0.00	2.4	0.99
Overall Well-being Score	0-10 Scale	9.0	2.7	4	10	0.00	2.3	0.99

[illegible]

2520 2530 2540 2550 2560
* * * * *
ACG CTC TCC TAC CGG GCG GAC TCG GAC GTC TTT GTG CCT TAT GGC TAC CTC TAC
Thr Leu Ser Tyr Arg Ala Asp Ser Asp Val Phe Val Pro Tyr Gly Tyr Leu Tyr

2570 2580 2590 2600 2610 2620
* * * * * *
CCC AGA AGC CAC CCC GGC GAC CCG CCC TCA GGC CTG SCC CCG CCA CTG TCC AGG
Pro Arg Ser His Pro Gly Asp Pro Pro Ser Gly Leu Ala Pro Pro Leu Ser Arg

2630 2640 2650 2660 2670
* * * * *
AAA CAG GGG CTG GTG GCA TGG GTG GTG AGC CAC TGG GAC GAG CGC CAG GCC CGG
Lys Gln Gly Leu Val Ala Trp Val Val Ser His Trp Asp Glu Arg Gln Ala Arg

2680 2690 2700 2710 2720 2730
* * * * * *
GTC CGC TAC TAC CAC CAA CTG AGC CAA CAT GTG ACC GTG GAC GTG TTC GGC CGG
Val Arg Tyr Tyr His Gln Leu Ser Gln His Val Thr Val Asp Val Phe Gly Arg

2740 2750 2760 2770 2780
* * * * *
GGC GGG CGG GGG CAG CGG GTG CCC GAA ATT GGG CTC CTG CAC ACA GTG GCC CGG
Gly Gly Pro Gly Gln Pro Val Pro Glu Ile Gly Leu Leu His Thr Val Ala Arg

2790 2800 2810 2820 2830
* * * * *
TAC AAG TTC TAC CTG GCT TTC GAG AAC TCG CAG CAC CTG GAT TAT ATC ACC GAG
Tyr Lys Phe Tyr Leu Ala Phe Glu Asn Ser Gln His Leu Asp Tyr Ile Thr Glu

2840 2850 2860 2870 2880 2890
* * * * * *
AAG CTC TGG CGC AAC GCG TTC CTC GCT GGG GCG GTG CCG GTG GTG CTG GGC CCA
Lys Leu Trp Arg Asn Ala Leu Leu Ala Gly Ala Val Pro Val Val Leu Gly Pro

2900 2910 2920 2930 2940
* * * * *
GAC CGT GCC AAC TAC GAG CGC TTT GTG CCC CGC GGC GCC TTC ATC CAC GTG GAC
Asp Arg Ala Asn Tyr Glu Arg Phe Val Pro Arg Gly Ala Phe Ile His Val Asp

2950 2960 2970 2980 2990 3000
* * * * * *
GAC TTC CCA AGT GCC TCC TCC CTG GCC TCG TAC CTG CTT TTC CTC GAC CGC AAC
Asp Phe Pro Ser Ala Ser Ser Leu Ala Ser Tyr Leu Leu Phe Leu Asp Arg Asn

3010 3020 3030 3040 3050
* * * * *
CCC GCG GTC TAT CGC CGC TAC TTC CAC TGG CGC CGG AGC TAC GCT GTC CAC ATC
Pro Ala Val Tyr Arg Arg Tyr Phe His Trp Arg Arg Ser Tyr Ala Val His Ile

3060 3070 3080 3090 3100
* * * * *
ACC TCC TTC TGG GAC GAG CCT TGG TGC CGG GTG TGC CAG GCT GTA CAG AGG GCT
Thr Ser Phe Trp Asp Glu Pro Trp Cys Arg Val Cys Gln Ala Val Gln Arg Ala

3110 3120 3130 3140 3150 3160
* * * * * *
GGG GAC CGG CCC AAG AGC ATA CGG AAC TTG GCC AGC TGG TTC GAG CGG TGA A
Gly Asp Arg Pro Lys Ser Ile Arg Asn Leu Ala Ser Trp Phe Glu Arg ***

Figure 4 (cont'd)

3170	3180	3190	3200	3210	3220
GCCGC	GCTCC	CCTGG	AAGCG	ACCCA	GGGGA
GGCCA	AGTTG	TCAGC	TTTTT	GATCC	TCTAC
3230	3240	3250	3260	3270	3280
TGTGC	ATCTC	CTTGA	CTGCC	GCATC	ATGGG
AGTAA	GTTCT	TCAAA	CACCC	ATTTT	TGCTC
3290	3300	3310	3320	3330	3340
TATGG	GAAAA	AAACG	ATTTA	CCAAT	TAATA
TTACT	CAGCA	CAGAG	ATGGG	GGCCC	GGTTT
3350	3360	3370	3380	3390	3400
CCATA	TTTTT	TGCAC	AGCTA	GCAAT	TGGGC
TCCCT	TTGCT	GCTGA	TGGGC	ATCAT	TGTTT
3410	3420	3430	3440	3450	3460
AGGGG	TCAAG	CAGGG	COTTC	TTCCT	CACCT
TGTAA	CCAGT	SCAGA	AATGA	AATAG	CTTAG
3470	3480	3490	3500	3510	3520
CGGCA	AGAAG	CCOTT	GAGGC	GSTTT	CCTGA
ATTTC	CCCAT	CTGCC	ACAGG	GCATA	TTTGT
3530	3540	3550	3560	3570	3580
GGCCC	GTGCA	GCTTC	CAAAAT	CTCAT	ACACA
ACTGT	TCCCG	ATTCA	CGTTT	TTCTG	GACCA
3590	3600	3610	3620	3630	3640
AGGTG	AAGCA	AATTT	GTGGT	TGTAG	AAGGA
GCCTT	GTGGG	TGGAG	AGTGG	AAGGA	CTGTG
GCTGC	AG				

104650 52465000

[illegible]

FIGURE 6

[illegible]

Figure 7 (page 1)

$\alpha(1,3)$ FT DNA (-128)	TTTTCTCA
$\alpha(1,3)$ FT DNA (-120)	TCTGTGAAACAGGAATAATACAGCTCTTCTCAGGACTCATGGCCTGGAGCTTTGGTAAG
$\alpha(1,3)$ FT DNA (-60)	CAGGAGATTGTCATCAATGACCCCTCACTCTCTCTCCCCACTTCCCAGAGACTCTGACCC
$\alpha(1,3)$ FT AA	M D P L G P A K P Q W S W R C C L T T L
$\alpha(1,3)$ FT DNA (1)	ATGGATCCCCCTGGGCCCCGCCAAGCCACAGTGGTGGCGCTGCTGTCTGACCCACGCTG
Lewis FT DNA	 ATGGATCCCCCTGGGTGCAGCCCAAGCCACAATGGCCATGGCGCGCTGTCTGGCCGCACTG
$\alpha(1,3)$ FT AA	L F Q L L M A V C F F S Y L R V S Q D D
$\alpha(1,3)$ FT DNA (61)	CTGTTTCAGCTGCTGATGGCTGTGTGTTTCTCTCCTATCTGCGTGTCTCAAGACGAT
Lewis FT DNA	 CTATTTTCAGCTGCTGTTGGCTGTGTGTTTCTCTCCTACCTGCGTGTCTCCGAGACGAT
$\alpha(1,3)$ FT AA	P T V Y P N G S R F P D S T G T P A H S
$\alpha(1,3)$ FT DNA (121)	CCCACGTGTACCCCTAATGGTCC...CGCTTCCCA..GACAGCACAGGACCCCGCCCACTCC
Lewis FT DNA	 GCCACTGGATCCCCCTAG.GGCTCCCAGTGGTCCCTCCCCGACAGGACACC.ACTCCCCACCCGCCCC
$\alpha(1,3)$ FT AA	I P L I L L W T W P F N K P I A L P R C
$\alpha(1,3)$ FT DNA (181)	ATCCCCCTGATCCTGCTGTGGACGTGGCCCTTTTAAACAACCCATAGCTCTGCCCGCTGC
Lewis FT DNA	 ACCTCCTGATCCTGCTATGGACATGGCCCTTTCCACATCCCTGTGGCTCTGTCCCGCTGT
$\alpha(1,3)$ FT AA	S E M V P G T A D C N I T A D R K V Y P
$\alpha(1,3)$ FT DNA (241)	TCAGAGATGGTGCCTGGCACGGCTGACTGCAACATCACTGCCGACCCGCAAGGTGTATCCA
Lewis FT DNA	 TCAGAGATGGTGCCTGGCACAGCCGACTGCCACATCACTGCCGACCCGCAAGGTGTATCCA

Figure 7 (page 2)

$\alpha(1,3)$ FT AA	Q A D A V I V H H R E V M Y N P S A Q L
$\alpha(1,3)$ FT DNA (301)	CAGGCAGACGGTCTATCGTGCACCCAGAGGTCTATACAAACCCAGTGCCCCAGCTC
Lewis FT DNA	
$\alpha(1,3)$ FT AA	P R S P R R Q G Q R W I W F S M E S P S
$\alpha(1,3)$ FT DNA (361)	CCACGCTCCCCGAGGGCGGCGAGGATCTGGTTACGATGGAGTCCCAAGC
Lewis FT DNA	
$\alpha(1,3)$ FT AA	H C W Q L K A M D G Y F N L T M S Y R S
$\alpha(1,3)$ FT DNA (421)	CACTGTGGCAGCTGAAAGCCATGGACGGATACTTCAATCTCACCATGTCTACCGCAGC
Lewis FT DNA	
$\alpha(1,3)$ FT AA	D S D I F T P Y G W L E P W S G Q P A H
$\alpha(1,3)$ FT DNA (481)	GACTCCGACATCTTCACGCCCTACGGCTGGCTGGAGCCGTGGTCCGGCCAGCCTGCCAC
Lewis FT DNA	
$\alpha(1,3)$ FT AA	P P L N L S A K T E L V A W A V S N W G
$\alpha(1,3)$ FT DNA (541)	CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCCTGGGAGTGTCCAACTGGGG
Lewis FT DNA	
$\alpha(1,3)$ FT AA	P N S A R V R Y Y Q S L Q A H L K V D V
$\alpha(1,3)$ FT DNA (601)	CCAACTCCGCCAGGTGGCTACTACCAGAGCCTGCAGGCCCATCTCAAGTGGACGTG
Lewis FT DNA	

Figure 7 (page 4)

GAGGCTGGTGTGGGGCCCTGGGCTGCCAGGAACCTCATTTTCCTGGGGCCCTCACCTGAGTG
 GGGGCCCTCATCTACCTAAGGACTCGTTTGCCCTGAAGCTTCACCTGCCCTGAGGACTCACCT
 GCCTGGGACGGTCACCTGTTGCAGCTTCACCTGCCCTGGGATTCACCTACCTGGGTCCTC
 ACTTTCCTGGGGCCCTCACCTGCTGGAGTCTTCGGTGGCCAGGTATGTCCTTACCTGGGA
 TTTACATGCTGGCTTCCAGGAGCGTCCCCCTGCGGAAGCCCTGGCCCTGCTGGGATGTCTC
 CTGGGGACTTTGGCCTACTGGGGACCTCGGCTGTTGGGGACTTTACCTGCTGGGACCTGCT
 CCCAGAGACCTTCCACACTGAATCTCACCTGCTAGGAGCCTCACCTGCTGGGGACCTCAC
 CCTGGAGGCACTGGGGCCCTGGGAACT

Figure 8.

